

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 28, 2003, 15:26:12 ; Search time 94 Seconds
(without alignments)
2591.952 Million cell updates/sec.

Title: US-09-868-987-14
Perfect score: 2778
Sequence: 1 MVSSPILNVLKPNHASVSGK.....SLYIAPLLLPVVRKRNRSK 552

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0
Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=Issued Patents NA -QWMT=fastcap -SUFFIX=rni -MINWATCH=0.1 -LOOFCCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
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-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:
1: /cgn2_6/ptodata/2/ina/5A.COMB.seq:
2: /cgn2_6/ptodata/2/ina/5B.COMB.seq:
3: /cgn2_6/ptodata/2/ina/6A.COMB.seq:
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq:
5: /cgn2_6/ptodata/2/ina/PTUS.COMB.seq:
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	2730	98.3	1230025	4	US-09-198-452A-1
C 2	719	25.9	1830121	4	US-09-557-884-1
C 3	719	25.9	1830121	4	US-09-643-990A-1
C 4	678.5	24.4	2211	3	US-09-462-844-1
C 5	672	24.2	6321	4	US-09-221-017B-311
C 6	646.5	23.3	2301	4	US-09-134-001C-852
C 7	512	18.4	4403765	3	US-09-103-840A-2
C 8	509	18.3	4411529	3	US-09-103-840A-1
C 9	483.5	17.4	40429	4	US-08-311-731A-125
C 10	425	15.3	1398	4	US-09-252-991A-6413
C 11	418	15.0	1947	4	US-09-328-352-1027
C 12	417	15.0	1890	4	US-09-252-991A-6330

C 13	369.5	13.3	969	4	US-09-352-991A-6245	Sequence 6245, Ap
C 14	369.5	13.3	984	4	US-09-252-991A-6054	Sequence 6054, Ap
C 15	358	12.9	429	4	US-09-352-991A-6217	Sequence 6217, Ap
C 16	314	11.3	870	4	US-09-352-991A-6138	Sequence 6138, Ap
C 17	306.5	11.0	996	4	US-09-328-352-1243	Sequence 1243, Ap
C 18	170.5	6.1	1664976	4	US-08-916-421B-1	Sequence 1, Appli
C 19	138	5.0	3102	4	US-09-252-991A-4040	Sequence 4040, Ap
C 20	138	5.0	4284	4	US-09-252-991A-4006	Sequence 4006, Ap
C 21	138	5.0	4704	4	US-09-252-991A-3906	Sequence 3906, Ap
C 22	137.5	4.9	3120	4	US-09-328-352-1348	Sequence 1348, Ap
C 23	136	4.9	3096	5	PCT-US96-05320A-897	Sequence 897, App
C 24	136	4.9	3156	4	US-09-134-001C-2168	Sequence 2168, Ap
C 25	136	4.9	1830121	4	US-09-557-884-1	Sequence 1, Appli
C 26	132	4.8	1830121	4	US-09-643-990A-1	Sequence 1, Appli
C 27	132	4.8	1664976	4	US-08-916-421B-1	Sequence 1, Appli
C 28	128.5	4.6	3201	4	US-09-352-991A-14959	Sequence 14959, A
C 29	128.5	4.6	3402	4	US-09-252-991A-14791	Sequence 14791, A
C 30	127	4.6	288	4	US-09-134-001C-829	Sequence 829, App
C 31	126.5	4.6	15393	4	US-09-453-702B-191	Sequence 191, App
C 32	124	4.5	3003	4	US-09-252-991A-14790	Sequence 14790, A
C 33	124	4.5	3132	4	US-09-252-991A-14540	Sequence 14540, A
C 34	124	4.5	3411	4	US-09-352-991A-14823	Sequence 14823, A
C 35	123.5	4.4	2862	4	US-09-352-991A-443	Sequence 443, App
C 36	123.5	4.4	3102	4	US-09-328-352-1012	Sequence 1012, App
C 37	123.5	4.4	3156	4	US-09-252-991A-418	Sequence 418, App
C 38	123	4.4	2862	4	US-09-252-991A-10659	Sequence 10659, A
C 39	123	4.4	2910	4	US-09-352-991A-10414	Sequence 10414, A
C 40	123	4.4	3111	4	US-09-352-991A-10504	Sequence 10504, A
C 41	122.5	4.4	1713	4	US-09-252-991A-14948	Sequence 14948, A
C 42	122.5	4.4	3144	4	US-09-252-991A-14688	Sequence 14688, A
C 43	122.5	4.4	3198	4	US-09-252-991A-15066	Sequence 15066, A
C 44	121.5	4.4	3186	4	US-09-328-352-319	Sequence 319, App
C 45	118.5	4.3	7886	4	US-09-453-702B-102	Sequence 102, App

ALIGNMENTS

RESULT 1
US-09-198-452A-1/c
; Sequence 1, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment thereof and uses thereof, in particular for the diagnosis, prev
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1
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Alignment Scores:
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 Best Local Similarity: 99.28% Mismatches: 1
 Query Match: 99.27% Indels: 3
 DB: 4 Gaps: 0

US-09-868-987-14 (1-552) x US-09-198-452A-1 (1-1230025)

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 QY 21 PheThrHisArgGluValSerLysLeuAlaSerAspLeuLysSerGlyAlaMetSerPhe 40
 DB 661846 TTTACCCACCGTGAAGTCAGCAAACTCGCCCTCAGATTATAAATCTGGAGCGATGCTTTT 661787
 QY 41 ValProGluValLeuSerGluGluThrIleSerSerAspLeuGlyLysGlnCysThr 60
 DB 661786 GTTCCCGAGGTTCTCAGTGAAGACGATCTCTTCGATCTTGGAAAAACAATGTACA 661727
 QY 61 GlnGlyIlelleSerAlaCysGlyLeuAlaMetLeuIleValLeuMetSerValTyr 80
 DB 661726 CAAGCCATTATCTCAGCATGCTGTGGCTTGGCAATGCTTATTGTTTGTGATGAGGTATAT 661667
 QY 81 TyrArgPheGlyGlyValIleAlaSerGlyAlaValLeuLeuLeuLeuLeuLeuLeu 100
 DB 661666 TATAGATTGGAGCGCTCATCGCTTCGGAGCTGTTCTTCTGAATCTTTTGTCTATCTGG 661607
 QY 101 AlaAlaLeuGlnTyrLeuAspAlaProLeuThrLeuSerGlyLeuAlaGlyIleValLeu 120
 DB 661606 GCAGCTCTACAGATTATGGATGGCCACTCACCTTGTTCAGACTCTCGTGGATTGTTCTT 661547
 QY 121 AlaMetGlyMetAlaValAlaAspAlaAsnValLeuValPheGluArgIleArgGluPhe 140
 DB 661546 GCTATGGGGATGCCGTAGATGCAAAATGTTCTGTATTTCGAAAGATCCGAGAGGAATTT 661487
 QY 141 LeuLeuSerGlnSerLeuLysSerValGluLysGlyTyrThrLysAlaPheGlyAla 160
 DB 661486 TTATGTCTCAAGTCTTAAAAATCTGTAGAAAAAGGATATACCAAGGCTTTTGGAGCC 661427
 QY 161 IlePheAspSerAsnLeuThrValLeuAlaSerAlaLeuLeuPhePheLeuAspThr 180
 DB 661426 ATTTTGTATCTAACTTACATGATGTCCTCAGCACTCTTTTCTTCCTAGATACA 661367
 QY 181 GlyProIleLysGlyPheAlaLeuThrLeuLeuGlyIlePheSerSerMetPheThr 200
 DB 661366 GGGCCCTATTAAAGGGTTTGTCTTGGATGATTTAGGAATTTTCTCTTCAATGTTTACG 661307
 QY 201 AlaLeuPheMetThrLysPhePheMetLeuTyrMetAsnLysThrGlnHisThrGln 220

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 QY 241 LeuTrpAlaValSerGlySerValPheLeuLeuGlyCysValAlaLeuGlyPheGlyAla 260
 DB 661186 CTTTGGGCTGTTCTTGGAAAGTGTTTTCTTTAGGTTGCTCTCTCGGTTTGGAGCC 661127
 QY 261 TrpAsnSerValLeuGlyMetAspPheLysGlyTyrAlaPheThrPheAsnProLys 280
 DB 661126 TGGAAATTCGTTTGGGAATGGAATTTAAAGAGGGATGTCCTTTACCTTTTAAATCAAAA 661067
 QY 281 GluHisGlyIleSerAspValAlaGlnMetArgGlyLysValValHisLysLeuGlnGlu 300
 DB 661066 GAGCATGGCATCAGCGATGTTGCTCAATCGGTGCAAAAGTTGTGCATAAACTACAGAA 661007
 QY 301 AlaGlyLeuSerSerArgAspPheArgIleGlnThrPheGlySerSerGluLysIleLys 320
 DB 661006 GCTGGTCTTTCTCTAGAGACTTCGCTATTCAAACTTTGATCTTCAGAAAAAGATCAAA 660947
 QY 321 IleTyrPheSerAspLysAlaLeuSerTyrThr-LysGlnIleArgAlaSerLeuLeuLys 340
 DB 660946 ATCTATTTTGTATGATAAGCTTTTAAGCTATACATAAGCAGATACGAGCCTCTCTCTAAA 660887
 QY 340 sLeuThrIleMetSerTrpArg-TyrCysGlyIleValValArgAsnArgProArgPheL 360
 DB 660886 ATTAACGATCATGAGCTGGCGTTAGCTGTGGGATTGTTGTTCAGNAACAGCCCTAGATTTC 660827
 QY 360 euTyrGlyAsnSerLysArgAsnAlaLys-PheTrpSerLysValSerSerLysLeuSer 379
 DB 660826 TCTACGGAAACTCTAAACGAAAGCGCAAAATTTTGGTCAAAAGGTAAACAGCAACTATCG 660767
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 QY 420 AspLeuLeuAlaThrCysAlaValLeuPheIleAlaHisPhePheLeuLysLysIleGln 439
 DB 660646 GACCTTTGGCTACCTGTGCGAGTCTTGTATTATAGCACATTTCTTTTGAAGAAAAATCAA 660587
 QY 440 IleAspLeuGlnAlaIleGlyAlaLeuMetThrValLeuGlyTyrSerLeuAsnAsnThr 459
 DB 660586 ATAGATTTCGAGCCATTGCTTTTAAAGTGTATTGGGGTATTCTATTAAACAATACT 660527
 QY 460 LeuIlePheAspArgIleArgGluAspArgGlnAlaAsnLeuPheThrProMetHis 479
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 QY 520 PheIleMetThrIleGlyIleLeuLeuGlyThrLeuSerSerLeuTyrIleAlaProPro 539
 DB 660346 TTTATTATGACCATAGGATCTCTAGGAACCTTTATCGTCTCTTTATATGCACACCT 660287
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RESULT 2

US-09-557-884-1/c

; Sequence 1, Application US/09557884

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